RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/501.930 A
Source:	1FW/6 ,.
Date Processed by STIC:	. 12/12/06

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 12/12/2006
PATENT APPLICATION: US/10/501,930A TIME: 10:34:57

Input Set : A:\P25687.APP

Output Set: N:\CRF4\12122006\J501930A.raw

```
3 <110> APPLICANT: TAKASHIMA, SHOU
             TSUJIMOTO, MASAFUMI
             TSUJI, SHUICHI
      7 <120> TITLE OF INVENTION: GLYCOSYLATING ENZYME
     9 <130> FILE REFERENCE: P25687
    11 <140> CURRENT APPLICATION NUMBER: 10/501,930A
C--> 12 <141> CURRENT FILING DATE: 2005-03-17
    14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00883
    15 <151> PRIOR FILING DATE: 2003-01-30
    17 <150> PRIOR APPLICATION NUMBER: JP 2002-21159
    18 <151> PRIOR FILING DATE: 2002-01-30
    20 <150> PRIOR APPLICATION NUMBER: JP 2002-122673
    21 <151> PRIOR FILING DATE: 2002-04-24
    23 <160> NUMBER OF SEQ ID NOS: 36
    25 <170> SOFTWARE: PatentIn Ver. 3.3
    27 <210> SEQ ID NO: 1
    28 <211> LENGTH: 398
    29 <212> TYPE: PRT
    30 <213> ORGANISM: Mus sp.
    32 <400> SEQUENCE: 1
    33 Met Arg Ser Gly Gly Thr Leu Phe Ala Leu Ile Gly Ser Leu Met Leu
    36 Leu Leu Leu Arg Met Leu Trp Cys Pro Ala Asp Ala Pro Ala Arg
                    20
    39 Ser Arg Leu Leu Met Glu Gly Ser Arg Glu Asp Thr Ser Gly Thr Ser
                                     40
    42 Ala Ala Leu Lys Thr Leu Trp Ser Pro Thr Thr Pro Val Pro Arg Thr
                                 55
    45 Arg Asn Ser Thr Tyr Leu Asp Glu Lys Thr Thr Gln Ile Thr Glu Lys
                             70
                                                 75
    48 Cys Lys Asp Leu Gln Tyr Ser Leu Asn Ser Leu Ser Asn Lys Thr Arg
                         85
                                             90
    51 Arg Tyr Ser Glu Asp Asp Tyr Leu Gln Thr Ile Thr Asn Ile Gln Arg
    54 Cys Pro Trp Asn Arg Gln Ala Glu Glu Tyr Asp Asn Phe Arg Ala Lys
                                    120
               115
    57 Leu Ala Ser Cys Cys Asp Ala Ile Gln Asp Phe Val Val Ser Gln Asn
                                135
                                                    140
    60 Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys
                            150
    63 His Ile Pro Ile Arg Glu Asn Ile Phe His Met Phe Pro Val Ser Gln
                                            170
                        165
```

66 Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly

RAW SEQUENCE LISTING DATE: 12/12/2006
PATENT APPLICATION: US/10/501,930A TIME: 10:34:57

Input Set : A:\P25687.APP

Output Set: N:\CRF4\12122006\J501930A.raw

67				180					185					190			
	Glv	Tle	Len	Asn	Lvs	Ser	Len	Cvs		Δla	Glu	Tle	Asn		Ser	Asp	
70			195		_, _			200	U -1		0		205				
	Phe	Val		Arg	Cvs	Asn	Leu		Pro	Ile	Thr	Glv		Ala	Ser	Lvs	
73		210		5	-1-		215					220				-1	
	Asp		Glv	Ser	Lvs	Thr		Leu	٧al	Thr	٧al		Pro	Ser	Tle	Ile	
	225		- 1		-7-	230					235					240	
		Leu	Lvs	Tyr	Gln		Leu	Lvs	Glu	Lvs		Ala	Gln	Phe	Leu		
79			_1	-2-	245			-1		250					255		
	Asp	Ile	Ser	Thr	Tvr	Glv	Asp	Ala	Phe		Leu	Leu	Pro	Ala		Ser	
82				260	- 2 -				265					270			
	Tvr	Arq	Ala	Asn	Thr	Glv	Ile	Ser	Phe	Lvs	Val	Tvr	Gln		Leu	Lys	
85	-1-	J	275			2		280				- 2	285				
	Glu	Ser		Met	Ara	Gln	Lvs		Leu	Phe	Phe	His		Ara	Tvr	Leu	
88		290	-1-		5		295					300		9	-1-		
	Ara		Leu	Ala	Leu	Phe		Ara	Thr	Lvs	Glv		Thr	Ala	Tvr	Ara	
	305					310		9		-1-	315				-1-	320	
		Ser	Thr	Gly	Len		Tle	Ala	Ser	Val		Val	Glu	Len	Cvs		
94				U -1	325					330			010		335		
	Asn	Val	Lvs	Leu		Glv	Phe	Trp	Pro		Ser	Lvs	Thr	Ile		Asp	
97			-1~	340	-1-	 1			345			-1-		350		F	
-	Thr	Pro	Leu	Ser	His	His	Tvr	Tvr		Asn	Met	Leu	Pro		His	Glv	
100			35				-1 -	360	_				365	_		2	
		His			Pro	Lys	Glu	ı Tyı	Sei	Glr	Met	: Leı			ı His	Met	
103		370					375					380					
							J/-	,				301	,				
	Arc			e Leu	ı Lys	Lei			e Sei	Lys	Cys			. Ala	à		
109		Gly		e Leu	Lys	Let 390	ı Glr		e Sei	. Lys	Cys 395	Glı		Ala	ì		
109	385	Gly	/ Ile				ı Glr		e Sei	. Lys		Glı		Ala	ì		
109 109	385 3 <21	Gl ₃ ; .0> 8	7 Ile SEQ I	e Leu ID NO IH: 3): 2		ı Glr		e Sei	. Lys		Glı		Ala	ì		
109 109 109	385 3 <21 3 <21	Gly 5 .0> 8 .1> I	Z Ile SEQ : LENG:	D NC): 2 :166		ı Glr		e Sei	: Lys		Glı		Ala	a		
109 109 110	385 9 <21 0 <21 L <21	Gly 6 .0> 8 .1> I .2> 7	7 Ile SEQ : LENG: TYPE:	ID NO): 2 166	390	ı Glr		e Sei	: Lys		Glı		Ala	a		
109 109 110 111 112	385 9 <21 0 <21 L <21	Gly 0> 8 1> 1 2> 7 3> 0	Ile SEQ : LENG: TYPE: DRGAM	ID NO TH: 3 : DNA): 2 166	390	ı Glr		e Sei	Lys		Glı		↑ Ala	a		
109 109 110 111 112 114	385 3 <21 3 <21 4 <21 4 <22	Gl ₃ .0> 8 .1> I .2> 7 .3> 0	FEATU	ID NO TH: 3 : DNA): 2 :166 Mus	390 s sp.	ı Glr		e Sei	Lys		Glı		Ala	à		
109 109 110 111 112 114	385 385 385 385 385 385 385 385	Gly 30> S 1> I 12> T 3> C 20> H	FEATUAME,	ID NO TH: 3 : DNA NISM: JRE:	0: 2 166 Mus	390 s sp.	ı Glr	n Ph∈	e Sei	Lys		Glı		c Ala	à		
105 106 105 116 112 114 115 116	385 385 385 385 385 385 385 385	Gl ₃ 6 10 > 5 1 > 1 2 > 7 3 > 0 10 > 1 21 > 1	FEATUAME,	ID NO TH: 3 : DNA NISM: JRE:	0: 2 166 Mus CDS (77	390 s sp.	ı Glr	n Ph∈	e Sei	: Lys		Glı		c Ala	à		
105 106 116 117 112 114 115 116	385 385 39 <21 20 <21 40 <22 50 <22 50 <22 50 <23	Gly	FEQUI	ID NO TH: 3 : DNA NISM: JRE: /KEY: TION:	0: 2 166 Mus CDS (77	39(s sp.	1 Glr	n Phe			395	Glu	ı Thi			gcgagg	60
105 106 116 117 112 114 115 116	385 385 39 <21 30 <21 4 <22 4 <22 5 <22 5 <22 8 <40 9 cgg	Gly 60> S 1> I 2> T 3> C 10> I 10> S 10> S 100> S	FEATUAME, LOCATE SEQUE	ID NO TH: 3 : DNA NISM: JRE: /KEY: TION: TION:): 2 :166 Mus CDS (77 2	39(s sp.	1 Glr (1270	n Phe	ig cg	gette	395 :gccc	Glu	ı Thi	cttt	ggcg	gcgagg ta ggc	
105 106 116 117 112 114 115 116	385 385 385 385 385 385 385 385	Gly 60> S 1> I 2> T 3> C 10> I 10> S 10> S 100> S	FEATUAME, LOCATE SEQUE	ID NO TH: 3 : DNA NISM: JRE: /KEY: TION: TION:	O: 2 166 Mus CDS (77 2	390 3 sp. 3 3	i Glr (1270 geceg iga t) gggct	aga g	getto gge a	395 egeco	s Glu	gcago tc g	ettt gec (ggcç etc a	ıta ggc	112
105 106 116 112 114 115 116 118 123	5 385 9 <21 0 <21 1 <21 2 <21 1 <22 5 <22 5 <22 6 <22 6 <22 7 <22 8 <40 9 cgg	Gly 60> S 1> I 2> T 3> C 10> I 10> S 10> S 100> S	FEATUAME, LOCATE SEQUE	ID NO TH: 3 : DNA NISM: JRE: /KEY: TION: TION:	O: 2 166 Mus CDS (77 2	390 3 sp. 3 3	i Glr (1270 geceg iga t) gggct	aga g	getto gge a	395 egeco	s Glu	gcago tc g	ettt gec (ggcç etc a		112
105 106 116 112 114 115 116 118 122 123	5 385 9 <21 0 <21 1 <21 2 <21 4 <22 5 <22 5 <22 6 <22 1 acg	G Gly	FEQUIPMENT OF THE PROPERTY OF	ID NOTH: 3: DNANISM: VEY: VEY: VEY: SINCE: agto	O: 2 166 Mus CDS (77 2 eggte	390	(1270 geeeg iga t	gggct ggct cg g	313 0 33 3 3 6	gette gge a Bly T 5	395 egcco lcg c	e cgg	gcago tc o	ettt gec (Ala I	ggcg ctc a Leu I 10	ta ggc le Gly	112
105 106 116 117 117 118 118 121 122 123 125	5 385 9 <21 0 <21 1 <21 2 <21 4 <22 5 <22 5 <22 6 <40 9 cgg	Gly Gly	FEATURE SEQUENCE OF SEQUENCE O	ID NOTH: 3: DNATION: JRE: /KEY: TION: agto ctca	O: 2 166 Mus CDS (77 2 cggts	390 3 sp. 3 sp. 3 sp. 4 sp. 4 sp. 4 sp. 5 sp. 6 sp. 6 sp. 6 sp. 7 sp. 6	(1270) (1270) gcccg iga t arg s)) gggct cg c Ser C	d cat	gette gge a Sly T 5 : atg	egeco leg c lar I	e cgg	gcago tc g he 1	ettt gee o Ala I	ggcg etc a Leu I 10	ta ggc le Gly gac	112
105 106 116 117 117 118 118 121 122 123 125	5 385 9 <21 9 <21 1 <21 2 <21 1 <22 5 <22 6 <22 6 <22 6 <22 8 <40 9 cgg 1 acg 8 ago 8 Ser	Gly Gly	FEATURE SEQUENCE OF SEQUENCE O	ID NO FH: 3 ID NO	O: 2 166 Mus CDS (77 2 cggts	390 3 sp. 3 sp. 3 sp. 4 sp. 4 sp. 4 sp. 5 sp. 6 sp. 6 sp. 6 sp. 7 sp. 6	(1270) (1270) gcccg iga t arg s)) gggct cg c Ser C	gly ogt	gette gge a Sly T 5 : atg	egeco leg c lar I	e cgg	gcago tc g he 1	ettt gee o Ala I e ees s Pro	ggcg etc a Leu I 10	ta ggc le Gly	112
109 106 116 117 118 118 118 122 123 126 126 127	5 385 9 <21 0 <21 <21 <21 1 <22 5 <22 5 <22 6 <22 5 <22 5 <22 5 <22 5 <22 5 <22 5 <22 5 <22 5 <22 5 <22	Gly Gly	FEATO SEQUE	ID NO FH: 3 ID NO FH: 3 ID NO	D: 2 166 Mus CDS (77 2 sggts sgg a	390 s sp. sycc gate a let A let A let Let	(1270) gcccg iga t arg s	gggct gggct cg g Ger G	gly ogt	gette gge a Sly T 5 ato g Met	gccc icg c Thr I	e egg etg t Leu I	gcago tc g he A y tgo Cys	ettt gec o Ala I e ees s Pro	ggcg etc a seu I 10 a gcc o Ala	ta ggc le Gly gac Asp	112
109 106 116 117 118 118 118 129 129 129 129 129 129	5 385 9 <21 9 <21 <21 <21 4 <22 5 <22 6 <22 6 <22 6 <26 6 <26 7 gcg	Gly Gly	FEATO SEQUE	ID NO FH: 3 ID NO FH: 3 ID NO ID NO FE FION: GOOGLE	D: 2 166 Mus CDs (77 2 ggto	390 s sp. gcc control gct f	(1270) (1270) gcccg iga t irg s	gggct gggct cg g cer G c ctg Lei 20	cg cg ggg g Gly G g cgt n Arg	gette gge a Gly 1 5 atg Met	gccc lcg c lhr I ctc Leu	c cgg ctg t Leu I c tgg	gcago tc c he I g tgo Cys 25 c aga	cttt gcc (Ala I c cca G Pro	ggco ctc a Leu I 10 a gco o Ala	ta ggc le Gly gac Asp	160
109 106 116 117 118 118 118 129 129 129 129 129 129	5 385 9 <21 9 <21 1 <21 2 <21 4 <22 5 <22 6 <22 6 <22 6 <22 7 gcg 9 Ala	Gly Gly	FEATON AME, LOCATE BEQUE BE SERVED B	ID NO FH: 3 ID NO FH: 3 ID NO ID NO FE FION: GOOGLE	D: 2 166 Mus CDs (77 2 ggto	390 s sp. gcc control gct f	(1270) (1270) gcccg iga t irg s	gggct cg g c ctg Leu 20 g ttg	cg cg ggg g Gly G g cgt n Arg	gette gge a Gly 1 5 atg Met	gccc lcg c lhr I ctc Leu	c cgg ctg t Leu I c tgg	gcago ttc o Phe I g tgo Cys 25 25 25	cttt gcc (Ala I c cca G Pro	ggco ctc a Leu I 10 a gco o Ala	ta ggc le Gly gac Asp	160
109 106 116 117 118 118 118 129 129 129 130 131	5 385 9 <21 0 <21 1 <21 1 <22 5 <22 5 <22 6 <22 8 <40 9 cgg 2 acg	Gly Gly	FEATON AME, LOCATE BEQUE BE SERVED B	ID NO FH: 3 ID NO	D: 2 166 Mus CDS (77 2 2 2 2 2 3 4 4 4 4 5 4 5 5 6 5 6 7 7 7 7 8 7 8 7 8 8 8 8 8 8 8 8 8 8 8	390 s sp. gcc catg a let I g ctc l Let cagg Arg	(1270) (1	gggct cg g c ctg Leu 20 g ttg	gg cg ggg g gly c g cgt n Arg	gette gge a gly T s ate g Met g gae s Glu	gccc lcg c lhr I g ctc leu gga l Gly	c cgc ctg t Leu I c tgc i Trp i ago	gcago tto g Phe P g tgo Cys 25 c aga	ettt gec o Ala I e eca B Pro G a gao g Gli	ggcg ctc a Leu I 10 a gcc o Ala g gac	ta ggc le Gly gac Asp acc	160
109 106 116 117 118 118 129 129 129 130 131 133	5 385 9 <21 1 <21 2 <21 4 <22 5 <22 6 <22 6 <22 6 <22 7 accept	Gly Gly	FEATURE SEQUENCE SEQU	ID NO FH: 3 : DNF NISM: JRE: /KEY: FION: ENCE: agto ctca g ctg Leu 6 c cgc a Arg	D: 2 166 Mus CDS (77 2 2 2 2 3 3 4 4 5 4 5 4 5 5 6 6 7 7 7 8 7 8 7 8 8 8 8 8 8 8 8 8 8 8	s sp. gcc gatg a gt Arg	(1270) (1	gggct cg c c ctg Leu 20 ttg ttg	eg ce ggg g gly c g cgt n Are n ate	gette gge a Sly T s ato g Met g gag c Glu	gccc lcg c lhr I g ctc g Leu g gga l Gly	c cgg ctg t Leu I c tgg c Trr c ago v Ser 40	gcago ttc c the I g tgo Cys 25 aga T Arc	ettt gec (Ala I e eca s Pro s Qaq g Gli	ggcgetc a Leu I 10 a gcc a Ala g gac a Asp	ta ggc le Gly gac Asp acc Thr	112 160 208
109 106 110 111 112 114 118 119 120 120 120 120 130 131 133 134	5 385 (21) (21) (21) (21) (22) (22) (22) (22)	Gly Gly	FEATURE SEQUENCE SEQU	ID NO FH: 3 : DNF NISM: JRE: /KEY: FION: ENCE: agto ctca g ctg Leu 6 c cgc a Arg	D: 2 166 Mus CDS (77 2 2 2 2 3 3 4 4 5 4 5 4 5 5 6 6 7 7 7 8 7 8 7 8 8 8 8 8 8 8 8 8 8 8	s sp. gcc gatg a gt Arg	(1270) (1	gggct cg c c ctg Leu 20 ttg ttg	eg ce ggg g gly c g cgt n Are n ate	gette gge a Sly T s ato g Met g gag c Glu	gccc lcg c lhr I g ctc g Leu g gga l Gly	c cgg ctg t Leu I c tgg 1 Trp 1 ago 2 Ser 40	gcago ttc c the I g tgo Cys 25 aga T Arc	ettt gec (Ala I e eca s Pro s Qaq g Gli	ggcgetc a Leu I 10 a gcc a Ala g gac a Asp	ta ggc le Gly gac Asp acc	112 160 208
105 106 116 117 118 118 127 128 129 129 130 131 133 134 135	5 385	G Gly O S O S O S O S O S O S O S O	EEQ CLENGTYPE: DRGAN FEATURE LOCATE SEQUE	ID NO FH: 3 ENF: VEY: VEY: CON: CONCE: AGC CONCE	D: 2 166 Mus CDS (77 2 2 2 2 3 3 4 4 5 4 5 4 6 6 6 7 7 7 7 8 7 8 8 7 8 8 8 8 8 8 8 8	s sp. scool gcc gatg at a lear Arc	(1270) (1	ggct cg g cer c Leu 20 1 Leu 1 Leu 1 Lys	eg cg ggg g gly C g cgt n Arg n atg n Met g aca	gette gge a gly T s atg g Met g gag c Glu	gccc icg cc in I g ctc g ctc g gga g Gly g tgg	c cgg ctg t Leu I c tgg l Trp l ago y Ser d Ser	gcago ctc o Phe A g tgo c Cys c aga c Arc	ettt gec o Ala I e eca s Pro 6 a gao g Glu g aca o Thr	ggcgetc a Leu I 10 a gcc o Ala g gac a Asp	ta ggc le Gly gac Asp acc Thr	112 160 208

RAW SEQUENCE LISTING DATE: 12/12/2006
PATENT APPLICATION: US/10/501,930A TIME: 10:34:57

Input Set : A:\P25687.APP

Output Set: N:\CRF4\12122006\J501930A.raw

138 139	Val	Pro	Arg	Thr	Arg 65	Asn	Ser	Thr	Tyr	Leu 70	Asp	Glu	Lys	Thr	Thr 75	Gln	
141	ata	aca	qaq	aaa	tgc	aaa	gat	ctg	caa	tat	agc	ttg	aac	tct	tta	tct	352
142	Ile	Thr	Glu	Lys	Cys	Lys	Asp	Leu	Gln	Tyr	Ser	Leu	Asn	Ser	Leu	Ser	
143				80	•	-	_		85	_				90			
145	aac	aaa	acq	aqa	cqq	tac	tct	gag	gat	qac	tac	ctc	caq	acc	atc	aca	400
								Glu									
147		•	95	_	J	•		100	-	-	•		105				
149	aac	ata	caq	aqa	tgc	cca	tqq	aac	cgq	caa	gca	gaa	gaa	tat	gac	aat	448
			_	_	_			Asn			-						
151		110		J	•		115		•			120		-	_		
153	ttt	aqa	qca	aaa	ctg	gct	tcc	tgt	tgc	gat	gcc	att	caa	gac	ttc	gtg	496
								Cys									
155		_		•		130		•	-	_	135			_		140	
157	gtt	tcc	caq	aac	aac	act	cca	gtg	ggg	act	aac	atg	agc	tac	gag	gtg	544
								Val									
159					145				_	150				_	155		
161	gaa	agc	aag	aaa	cac	atc	ccc	att	cga	gag	aac	att	ttc	cac	atg	ttt	592
162	Ğlu	Ser	Lys	Lys	His	Ile	Pro	Ile	Arg	Glu	Asn	Ile	Phe	His	Met	Phe	
163			_	160					165					170			
165	cca	gtg	tcg	cag	cct	ttt	gtg	gac	tat	CCC	tat	aac	cag	tgt	gca	gtg	640
166	Pro	Val	Ser	Gln	Pro	Phe	Val	Asp	Tyr	Pro	Tyr	Asn	Gln	Cys	Ala	Val	
167			175					180					185				
								aac									688
170	Val	Gly	Asn	Gly	Gly	Ile	Leu	Asn	Lys	Ser	Leu	Cys	Gly	Ala	Glu	Ile	
171		190					195					200					
173	gat	aaa	tct	gac	ttc	gtc	ttc	agg	tgt	aac	ctc	CCC	cca	atc	aca	ggg	736
174	Asp	Lys	Ser	Asp	Phe	Val	Phe	Arg	Cys	Asn	Leu	Pro	Pro	Ile	Thr		
175						210					215					220	
								agc									784
178	Ser	Ala	Ser	Lys	Asp	Val	Gly	Ser	Lys		Asn	Leu	Val	Thr		Asn	
179					225					230					235		
								tac									832
	Pro	Ser	Ile		Thr	Leu	Lys	Tyr		Asn	Leu	Lys	Glu		Lys	Ala	
183				240		_			245		<i>^</i> .			250			000
								acc									880
	Gln	Phe		Glu	Asp	Ile	Ser	Thr	Tyr	Gly	Asp	Ala		Leu	Leu	Leu	
187			255					260					265				000
								aac									928
	Pro		Phe	Ser	Tyr	Arg		Asn	Thr	GIŸ	тте		Pne	ьys	vai	Tyr	
191		270					275					280					076
								atg									976
		Thr	ьeu	ьуs	GIU		ьуs	Met	Arg	GIN		vaı	Leu	Рпе	Pne		
195				-4		290					295		-		~~~	300	1024
								gct									1024
	Pro	arg	Tyr	ьeu		HIS	ьeu	Ala	ьeu		Trp	Arg	ınr	ьуѕ		val	
199					305	.				310				~+~	315	~+~	1072
								ggc									1072
202	inr	Ата	ıyr	arg	ьeu	ser	Inr	Gly	டeu	met	тте	Ala	ser	val	Ата	val	

RAW SEQUENCE LISTING DATE: 12/12/2006 PATENT APPLICATION: US/10/501,930A TIME: 10:34:57

Input Set : A:\P25687.APP

Output Set: N:\CRF4\12122006\J501930A.raw

203			320					325					330			
	gaa ct	a tat	gaa	aac	qtq	aag	ctc	tac	gga	ttc	tgg	cct	ttc	tct	aag	1120
	Glu Le															
207		335				-	340	•	•		-	345			-	
	act at	c qaa	qac	acc	cca	ctc	aqt	cac	cac	tac	tat	gat	aac	atq	tta	1168
	Thr Il															
211	35		-			355				•	360	•				
	cct aa	q cat	aat	ttc	cac	caq	atq	cct	aaa	qaa	tac	aqc	caa	atg	ctc	1216
	Pro Ly															
	365		-		370				•	375	•				380	
	cag ct	c cat	atq	aga	qqa	atc	ctc	aaa	ctq	caa	ttc	aqc	aaa	tgt	gaa	1264
	Gln Le															
219				385	•			•	390				-	395		
	acg go	t taa	acqtt	tct	taga	aqqaq	a at	taati	ttca	g ga	ggtg	gagt	gga	tgtgt	ca	1320
	Thr Al		•		_											
	cagcat		aaaaa	agcc	aa ta	aqaaq	gaage	g ca	caqa	qaaa	qcat	gaat	tta	caaa	geget	1380
	ctccca															
	ctcatt															
	aagtaa															
	gaatgo	_	_						_							
	actgtg															
	ttacac															
	gaaaca															
	cttctg															
	gtttct															
	tgcttt															
	gttcaa															
	taaaat															
	aagata															
	atcato															
	gatccc															
	aactag															
	cagcag															
260	tgtgag	gcta	cgct	aaaa	cc to	ctgc	gtag	gga	gaga	gtac	agt	gcate	gag	tgtg	gcggct	2460
262	tttgtc	caca	ctcg	tgaa	gg gi	tgagi	taatt	t ca	gagc	caat	caca	atca	caa	ggate	ggacac	2520
	acctaa															
266	aagcat	cagt	tttg	agta	aa a	tttga	agtag	g at	gttaa	aata	tgaa	acati	ttt .	ataco	ctctta	2640
268	ctaatg	tccc	accg	acac	ct ti	ttaai	tgtaa	a gca	acati	ttat	ttai	taag	gtt .	actt	gacatt	2700
270	aaatgo	ttat	gtct	gtata	at to	ctgti	tcato	c cat	tcgat	ttt	CCC	aaaa	agt .	aagag	gcatag	2760
272	gagatg	aggc	ctac	atgc	ca a	gaaa	actat	t aaa	attti	tact	ctti	taati	tct	tacti	gagcc	2820
274	agcttg	ttgt	ttate	caag	tg ci	tttti	ttgaa	a ga	gaca	gcac	cct	gtgaa	att	cttca	attctg	2880
276	atacag	tgtc	acct	tgtai	tt ta	aacat	tttgt	t aat	tgtt	gttt	caa	gttta	aca	tctct	ttcat	2940
	tctttt															
280	attttg	caaa	gggt	aaaa	gg c	tttti	ttgtt	taaa	ataaa	aata	aaat	ttai	tta	tttt	cttctg	3060
	atgaat												taa .	attai	ctcct	
284	agcaac	attg	gtca	cgtt	tc a	atcai	tgcta	a tta	agcaa	aaaa	aaaa	aaa				3166
287	<210>	SEQ 1	D NO	: 3												
288	<211>	LENGT	TH: 3	98												
289	<212>	TYPE:	PRT													

RAW SEQUENCE LISTING DATE: 12/12/2006
PATENT APPLICATION: US/10/501,930A TIME: 10:34:57

Input Set : A:\P25687.APP

Output Set: N:\CRF4\12122006\J501930A.raw

290 <213> ORGANISM: Homo sapiens 292 <400> SEQUENCE: 3 293 Met Arg Pro Gly Gly Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu 296 Leu Leu Leu Arg Leu Leu Trp Cys Pro Ala Asp Ala Pro Gly Arg 299 Ala Arg Ile Leu Val Glu Glu Ser Arg Glu Ala Thr His Gly Thr Pro 302 Ala Ala Leu Arg Thr Leu Arg Ser Pro Ala Thr Ala Val Pro Arg Ala 305 Thr Asn Ser Thr Tyr Leu Asn Glu Lys Ser Leu Gln Leu Thr Glu Lys 70 308 Cys Lys Asn Leu Gln Tyr Gly Ile Glu Ser Phe Ser Asn Lys Thr Lys 85 90 311 Gly Tyr Ser Glu Asn Asp Tyr Leu Gln Ile Ile Thr Asp Ile Gln Ser 105 314 Cys Pro Trp Lys Arg Gln Ala Glu Glu Tyr Ala Asn Phe Arg Ala Lys 315 115 120 317 Leu Ala Ser Cys Cys Asp Ala Val Gln Asn Phe Val Val Ser Gln Asn 135 320 Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys 155 150 323 Glu Ile Pro Ile Lys Lys Asn Ile Phe His Met Phe Pro Val Ser Gln 170 165 326 Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly 185 180 329 Gly Ile Leu Asn Lys Ser Leu Cys Gly Thr Glu Ile Asp Lys Ser Asp 330 195 200 332 Phe Val Phe Arg Cys Asn Leu Pro Pro Thr Thr Gly Asp Val Ser Lys 215 335 Asp Val Gly Ser Lys Thr Asn Leu Val Thr Ile Asn Pro Ser Ile Ile 338 Thr Leu Lys Tyr Gly Asn Leu Lys Glu Lys Lys Ala Leu Phe Leu Glu 245 341 Asp Ile Ala Thr Tyr Gly Asp Ala Phe Phe Phe Leu Pro Ala Phe Ser 265 344 Phe Arg Ala Asn Thr Gly Thr Ser Phe Lys Val Tyr Tyr Thr Leu Glu 345 275 280 347 Glu Ser Lys Ala Arg Gln Lys Val Leu Phe Phe His Pro Lys Tyr Leu 295 350 Lys Asp Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg 310 315 353 Leu Ser Thr Gly Leu Met Ile Thr Ser Val Ala Val Glu Leu Cys Lys 325 330 356 Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Val Glu Asp 345 359 Ile Pro Val Ser His His Tyr Tyr Asp Asn Lys Leu Pro Lys His Gly 360 362 Phe His Gln Met Pro Lys Glu Tyr Ser Gln Ile Leu Gln Leu His Met

VERIFICATION SUMMARY

DATE: 12/12/2006

PATENT APPLICATION: US/10/501,930A

TIME: 10:34:58

Input Set : A:\P25687.APP

Output Set: N:\CRF4\12122006\J501930A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date